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Frontiers Editorial Office,
Frontiers Media SA, Switzerland

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### SPECIALTY SECTION

This article was submitted to Evolutionary and Genomic Microbiology, a section of the journal Frontiers in Genetics

RECEIVED 02 August 2022 ACCEPTED 03 August 2022 PUBLISHED 29 August 2022

## CITATION

Jagirdar G, Elsner M, Scharf C, Simm S, Borucki K, Peter D, Lalk M, Methling K, Linnebacher M, Krohn M, Wolke C and Lendeckel U (2022), Corrigendum: Reexpression of tafazzin isoforms in TAZ-deficient C6 glioma cells restores cardiolipin composition but not proliferation rate and alterations in gene expression.

Front. Genet. 13:1009773.

doi: 10.3389/fgene.2022.1009773

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# Corrigendum: Re-expression of tafazzin isoforms in TAZ-deficient C6 glioma cells restores cardiolipin composition but not proliferation rate and alterations in gene expression

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# KEYWORDS

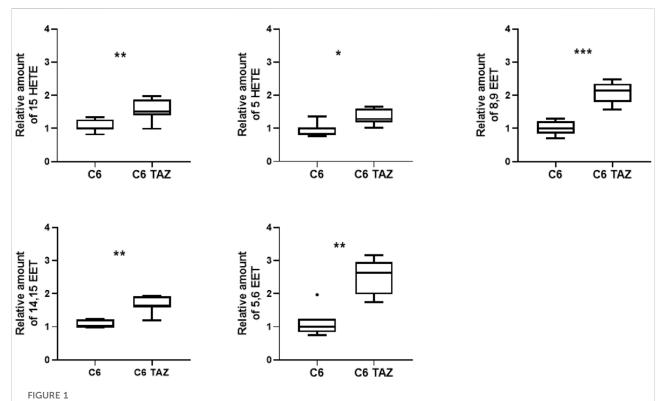
Barth syndrome, cardiolipin, cellular proliferation, gene expression, tafazzin, Barth syndrome (BTHS)

# A Corrigendum on

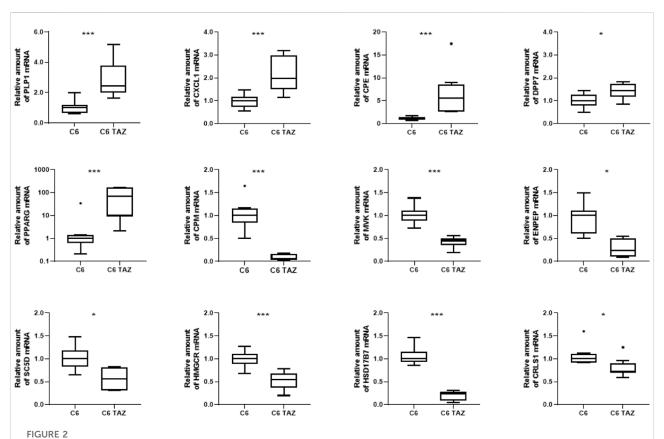
Re-expression of tafazzin isoforms in TAZ-deficient C6 glioma cells restores cardiolipin composition but not proliferation rate and alterations in gene expression

by Jagirdar G, Elsner M, Scharf C, Simm S, Borucki K, Peter D, Lalk M, Methling K, Linnebacher M, Krohn M, Wolke C and Lendeckel U (2022). Front. Genet. 13:931017. doi: 10.3389/fgene. 2022.931017

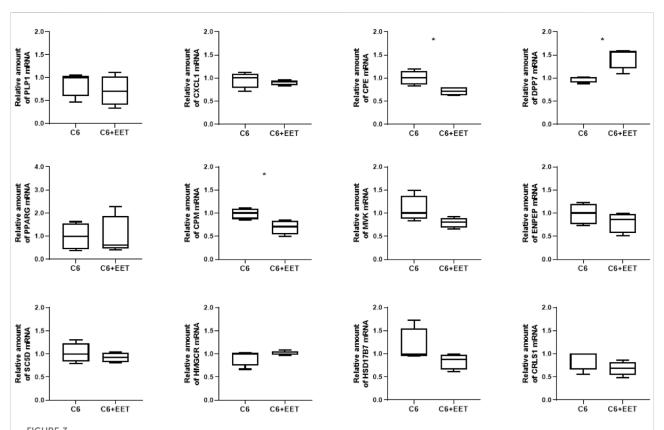
In the published article, there was an error in "Figures 1–5 and Table 1" as published. The figures were not in correct order and some human primers shown in Table 1 were not used in the study. The corrected figures and tables appear below.



Tafazzin deficiency alters oxylipin levels in C6 cells: Effect of tafazzin knockout on cellular lipids, oxylipins was determined by HPLC-MS/MS. The Data analysis was performed with Agilent Mass Hunter Qualitative and Quantitative Analysis software (version B.08.00 for both). For all detected oxylipins, a relative quantification was done by normalizing the area of the metabolite signal to the area of the signal of the internal standard compound (relative amount). Data is represented as median, quartile and interquartile range for n = 4.



Tafazzin deficiency alters gene expression in C6 cells: Quantification levels of indicated genes in C6 and C6 TAZ cells was preformed and the amount of mRNA was determined by using RT-qPCR and normalized to RPL13a. Data is given as boxplot with median, quartile, and interquartile range (\*p < 0.05; \*\*p < 0.01; \*\*\*p < 0.001). Outliers are indicated using Tukey method. n = 8.



Oxylipins regulates TAZ dependent gene expression in C6 cells: Relative gene expression of C6 cells treated with ethanol (control) and C6 cells with 3  $\mu$ M EET incubated at 37°C for 24 h. The amount of Mrna is determined by qpcr that is normalized to RPL13a. Data is represented as boxplot with median, quartile and interquartile range. Asterisks represent significant change.

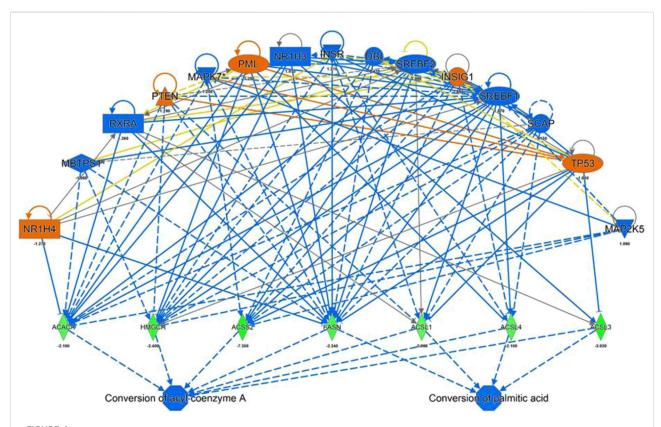


FIGURE 4

IPA Upstream Regulators Analysis for identification of upstream regulators that may be responsible for changes in gene expression observed for ACACA, HMGCR, ACSS2, FASN, ACSL 1,3 and 4 (predicted activation (orange) predicted inhibition (blue) of the regulators leads to a decreased expression (green)).

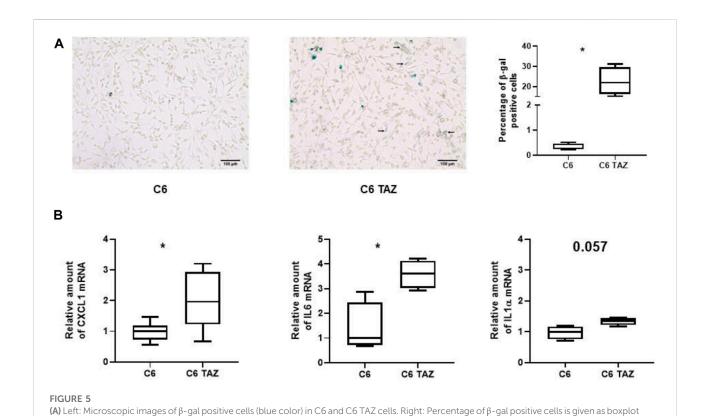


TABLE 1 List of primers used in the study.

normalized to RPL13a; n = 4, p = 0.029).

| Gene     | Upstream                    | Downstream                    |
|----------|-----------------------------|-------------------------------|
| rPLP1    | GCC CTG ACT GTT GTA TGG CT  | AGG GAA ACT AGT GTG GCT GC    |
| rCXCL1   | CTG CAC CCA AAC CGA AGT CA  | GAC GCC ATC GGT GCA ATC TA    |
| rCPE     | ACC TCC CTG TCG CAA GAA TG  | CCA TCC TTA GCC GAG GTG AC    |
| rDPP7    | GGG GAG CAC ATC ACC TAG AC  | GAA GGC TGC TAC TTA GGC CC    |
| rPPARG   | TCA AAG TAG AGC CTG CGT CC  | TGG CAT TGT GAG ACA TCC CC    |
| rCPM     | CGA GGC AAG ATT GAC CCA GT  | CAG CTC GTT TCC TTT CAC GC    |
| rMVK     | TCA TGG TGT GGT CGG AAC TG  | GGT ACT TCG TGG GAC CTT GG    |
| rENPEP   | CCT CAC ATC CGG TGG TTG TC  | TGG GTG ACG TTC TGC TTT CC    |
| rSC5D    | GAC CCT GGC AGC ACT GTA AT  | GGT CGG CTT TCC TGG CTA AT    |
| rHMGCR   | TAG AGA TCG GAA CCG TGG GT  | GCC CGT GTT TCA GTC CAG TA    |
| rHSD17B7 | CTG ACC AAA TAC TTG AGC GGC | TAG GAG GAG AGA TCA TCA TGG C |
| rCRLS1   | GCA TTC ACT ACA GCT GCG TC  | GCT GAA CAC CAA GAT CGG GA    |
| rIL6     | TCA TTC TGT CTC GAG CCC AC  | GTC TCC TCT CCG GAC TTG TG    |
| rILa     | AGT GGA ACC AGC CCG ACA TA  | TAT CCT ACC CAT CCG GCA CT    |
| RPLP13a  | CTG GTA CTT CCA CCC GAC CTC | GGA TCC CTC CAC CCT ATG ACA   |

(\* indicates p < 0.05). (B) Upregulation of SASP genes: Amounts of mrnas of CXCL1, IL6, and IL1 $\alpha$  are elevated in C6 TAZ cells (mrna expression

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